10/789,400

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(FILE 'HOME' ENTERED AT 19:45:33 ON 14 DEC 2006)

FILE 'MEDLINE, CAPLUS, BIOSIS, SCISEARCH, LIFESCI' ENTERED AT 19:46:14 ON 14 DEC 2006

L1 1238 S HUMAN(3A)METAPNEUMOVIRUS OR HMPV
L2 40 S (ABLAT? OR DISRUPT? OR REDUC? OR DECREAS? OR KNOCKOUT)(7A)M2-
L3 9 S L1 AND L2
L4 2 DUP REM L3 (7 DUPLICATES REMOVED)

=> d bib ab 1-2 l4

L4 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1
AN 2005:1056220 CAPLUS
DN 143:455706
TI Infection of nonhuman primates with recombinant human metapneumovirus lacking the SH, G, or M2-2 protein categorizes each as a nonessential accessory protein and identifies vaccine candidates
AU Biacchesi, Stephane; Pham, Quynh N.; Skiadopoulos, Mario H.; Murphy, Brian R.; Collins, Peter L.; Buchholz, Ursula J.
CS Laboratory of Infectious Diseases, National Institute of Allergy and Infectious Diseases, Bethesda, MD, 20892-8007, USA
SO Journal of Virology (2005), 79(19), 12608-12613
CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB Recombinant human metapneumovirus (HMPV) in which the SH, G, or M2 gene or open reading frame was deleted by reverse genetics was evaluated for replication and vaccine efficacy following topical administration to the respiratory tract of African green monkeys, a permissive primate host. Replication of the ΔSH virus was only marginally less efficient than that of wild-type HMPV, whereas the ΔG and Δ M2-2 viruses were reduced sixfold and 160-fold in the upper respiratory tract and 3,200-fold and 4,000-fold in the lower respiratory tract, resp. Even with the highly attenuated mutants, there was unequivocal HMPV replication at each anatomical site in each animal. Thus, none of these three proteins is essential for HMPV replication in a primate host, although G and M2-2 increased the efficiency of replication. Each gene-deletion virus was highly immunogenic and protective against wild-type HMPV challenge. The ΔG and ΔM2-2 viruses are promising vaccine candidates that are based on independent mechanisms of attenuation and are appropriate for clin. evaluation.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 2 MEDLINE on STN DUPLICATE 2
AN 2005251846 MEDLINE
DN PubMed ID: 15890897
TI Deletion of M2 gene open reading frames 1 and 2 of human metapneumovirus: effects on RNA synthesis, attenuation, and immunogenicity.
AU Buchholz Ursula J; Biacchesi Stephane; Pham Quynh N; Tran Kim C; Yang Lijuan; Luongo Cindy L; Skiadopoulos Mario H; Murphy Brian R; Collins Peter L
CS Laboratory of Infectious Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892-8007, USA.. ubuchholz@niaid.nih.gov
SO Journal of virology, (2005 Jun) Vol. 79, No. 11, pp. 6588-97.
Journal code: 0113724. ISSN: 0022-538X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)

LA English
FS Priority Journals
EM 200506
ED Entered STN: 14 May 2005
Last Updated on STN: 15 Jun 2005
Entered Medline: 14 Jun 2005
AB The M2 gene of human metapneumovirus (HMPV) contains two overlapping open reading frames (ORFs), M2-1 and M2-2. The expression of separate M2-1 and M2-2 proteins from these ORFs was confirmed, and recombinant HMPVs were recovered in which expression of M2-1 and M2-2 was ablated individually or together [rdeltaM2-1, rdeltaM2-2, and rdeltaM2(1+2)]. Each M2 mutant virus directed efficient multicycle growth in Vero cells. The ability to recover HMPV lacking M2-1 contrasts with human respiratory syncytial virus, for which M2-1 is an essential transcription factor. Expression of the downstream HMPV M2-2 ORF was not reduced when translation of the upstream M2-1 ORF was silenced, indicating that it is initiated separately. The rdeltaM2-2 mutants exhibited a two- to fivefold increase in the accumulation of mRNA, normalized to the genome template, suggesting that M2-2 has a role in regulating RNA synthesis. Replication and immunogenicity were tested in hamsters. Animals infected intranasally with rdeltaM2-1 or rdeltaM2(1+2) did not have recoverable virus in the lungs or nasal turbinates on days 3 or 5 postinfection and did not develop HMPV-neutralizing serum antibodies or resistance to HMPV challenge. Thus, M2-1 appears to be essential for significant virus replication in vivo. In animals infected with rdeltaM2-2, virus was recovered from only 1 of 12 animals and only in the nasal turbinates on a single day. However, all of the animals developed a high titer of HMPV-neutralizing serum antibodies and were highly protected against challenge with wild-type HMPV. The HMPV rdeltaM2-2 virus is a promising and highly attenuated HMPV vaccine candidate.

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(FILE 'HOME' ENTERED AT 14:45:15 ON 18 DEC 2006)

FILE 'MEDLINE, CAPLUS, BIOSIS, SCISEARCH, LIFESCI' ENTERED AT 14:45:58 ON 18 DEC 2006

L1 1202 S HUMAN(W)METAPNEUMOVIRUS
L2 1802 S M2-2
L3 29 S L1(P)L2
L4 10 DUP REM L3 (19 DUPLICATES REMOVED)

=> d au ti so pi ab 1-10 l4

L4 ANSWER 1 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AU Herd, Karen A.; Mahalingam, Suresh; Mackay, Ian M.; Nissen, Michael; Sloots, Theo P.; Tindle, Robert W.
TI Cytotoxic T-lymphocyte epitope vaccination protects against human metapneumovirus infection and disease in mice
SO Journal of Virology (2006), 80(4), 2034-2044
CODEN: JOVIAM; ISSN: 0022-538X
AB Human metapneumovirus (hMPV) has emerged as an important human respiratory pathogen causing upper and lower respiratory tract infections in young children and older adults. In addition, hMPV infection is associated with asthma exacerbation in young children. Recent epidemiol. evidence indicates that hMPV may cocirculate with human respiratory syncytial virus (hRSV) and mediate clin. disease similar to that seen with hRSV. Therefore, a vaccine for hMPV is highly desirable. In the present study, we used predictive bioinformatics, peptide immunization, and functional T-cell assays to define hMPV cytotoxic T-lymphocyte (CTL) epitopes recognized by mouse T cells restricted through several major histocompatibility complex class I alleles, including HLA-A*0201. We demonstrate that peptide immunization with hMPV CTL epitopes reduces viral load and immunopathol. in the lungs of hMPV-challenged mice and enhances the expression of Th1-type cytokines (gamma interferon and interleukin-12 [IL-12]) in lungs and regional lymph nodes. In addition, we show that levels of Th2-type cytokines (IL-10 and IL-4) are significantly lower in hMPV CTL epitope-vaccinated mice challenged with hMPV. These results demonstrate for the first time the efficacy of an hMPV CTL epitope vaccine in the control of hMPV infection in a murine model.

L4 ANSWER 2 OF 10 MEDLINE on STN DUPLICATE 1
AU Biacchesi Stephane; Pham Quynh N; Skiadopoulos Mario H; Murphy Brian R; Collins Peter L; Buchholz Ursula J
TI Infection of nonhuman primates with recombinant human metapneumovirus lacking the SH, G, or M2-2 protein categorizes each as a nonessential accessory protein and identifies vaccine candidates.
SO Journal of virology, (2005 Oct) Vol. 79, No. 19, pp. 12608-13.
Journal code: 0113724. ISSN: 0022-538X.
AB Recombinant human metapneumovirus (HMPV) in which the SH, G, or M2 gene or open reading frame was deleted by reverse genetics was evaluated for replication and vaccine efficacy following topical administration to the respiratory tract of African green monkeys, a permissive primate host. Replication of the deltaSH virus was only marginally less efficient than that of wild-type HMPV, whereas the deltaG and deltaM2-2 viruses were reduced sixfold and 160-fold in the upper respiratory tract and 3,200-fold and 4,000-fold in the lower respiratory tract, respectively. Even with the highly attenuated mutants, there was unequivocal HMPV replication at each anatomical site in each animal. Thus, none of these three proteins is essential for HMPV replication in a primate host, although G and M2-2 increased the efficiency of replication. Each gene-deletion virus was highly immunogenic and protective against wild-type HMPV challenge. The deltaG and deltaM2-2 viruses are promising vaccine candidates that are based on

independent mechanisms of attenuation and are appropriate for clinical evaluation.

L4 ANSWER 3 OF 10 MEDLINE on STN DUPLICATE 2
AU Buchholz Ursula J; Biacchesi Stephane; Pham Quynh N; Tran Kim C; Yang Lijuan; Luongo Cindy L; Skiadopoulos Mario H; Murphy Brian R; Collins Peter L
TI Deletion of M2 gene open reading frames 1 and 2 of human metapneumovirus: effects on RNA synthesis, attenuation, and immunogenicity.
SO Journal of virology, (2005 Jun) Vol. 79, No. 11, pp. 6588-97.
Journal code: 0113724. ISSN: 0022-538X.
AB The M2 gene of human metapneumovirus (HMPV) contains two overlapping open reading frames (ORFs), M2-1 and M2-2. The expression of separate M2-1 and M2-2 proteins from these ORFs was confirmed, and recombinant HMPVs were recovered in which expression of M2-1 and M2-2 was ablated individually or together [rdeltaM2-1, rdeltaM2-2, and rdeltaM2(1+2)]. Each M2 mutant virus directed efficient multicycle growth in Vero cells. The ability to recover HMPV lacking M2-1 contrasts with human respiratory syncytial virus, for which M2-1 is an essential transcription factor. Expression of the downstream HMPV M2-2 ORF was not reduced when translation of the upstream M2-1 ORF was silenced, indicating that it is initiated separately. The rdeltaM2-2 mutants exhibited a two- to fivefold increase in the accumulation of mRNA, normalized to the genome template, suggesting that M2-2 has a role in regulating RNA synthesis. Replication and immunogenicity were tested in hamsters. Animals infected intranasally with rdeltaM2-1 or rdeltaM2(1+2) did not have recoverable virus in the lungs or nasal turbinates on days 3 or 5 postinfection and did not develop HMPV-neutralizing serum antibodies or resistance to HMPV challenge. Thus, M2-1 appears to be essential for significant virus replication in vivo. In animals infected with rdeltaM2-2, virus was recovered from only 1 of 12 animals and only in the nasal turbinates on a single day. However, all of the animals developed a high titer of HMPV-neutralizing serum antibodies and were highly protected against challenge with wild-type HMPV. The HMPV rdeltaM2-2 virus is a promising and highly attenuated HMPV vaccine candidate.

L4 ANSWER 4 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
IN Haller, Aurelia; Tang, Roderick; Fouchier, Ronaldus Adrianus Maria; Van Den Hoogen, Bernadetta Gerarda; Osterhaus, Albertus Dominicus Marcellinus Erasmus
TI Human Metapneumovirus strains and their use in vaccine formulations and as vectors for expression of antigenic sequences, and methods for propagating virus
SO PCT Int. Appl., 613 pp.
CODEN: PIXXD2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2004096993	A2	20041111	WO 2004-US12724	20040423
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2004235347	A1	20041111	AU 2004-235347	20040423
CA 2523319	A1	20041111	CA 2004-2523319	20040423
US 2005019891	A1	20050127	US 2004-831780	20040423

EP 1623006 A2 20060208 EP 2004-750614 20040423
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK, HR

AB The present invention provides an isolated mammalian neg. strand RNA virus, metapneumovirus (MPV), within the sub-family Pneumoviridae, of the family Paramyxoviridae. The invention also provides isolated mammalian neg. strand RNA viruses identifiable as phylogenetically corresponding or relating to the genus Metapneumovirus and components thereof. In particular the invention provides a mammalian MPV, subgroups and variants thereof. The invention relates to genomic nucleotide sequences of different isolates of mammalian metapneumoviruses, in particular human metapneumoviruses (hMPV). The invention relates to the use of the sequence information of different isolates of mammalian metapneumoviruses for diagnostic and therapeutic methods. The present invention relates to nucleotide sequences encoding the genome of a metapneumovirus or a portion thereof, including both mammalian and avian metapneumovirus. The invention further encompasses chimeric or recombinant viruses encoded by said nucleotide sequences. The invention also relates to chimeric and recombinant mammalian MPV that comprise one or more non-native or heterologous sequences. The invention further relates to vaccine formulations comprising mammalian or avian metapneumovirus, including recombinant and chimeric forms said viruses. The vaccine prepns. of the invention encompass multivalent vaccines, including bivalent and trivalent vaccine prepns. The invention also provide methods for propagating virus.

L4 ANSWER 5 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN

IN Collins, Peter L.; Biacchesi, Stephane; Buchholz, Ursula; Skiadopoulos, Mario H.; Murphy, Brian R.

TI Recombinant human metapneumovirus comprising attenuating nucleotide modifications and its use for eliciting an immune response

SO U.S. Pat. Appl. Publ., 190 pp.
CODEN: USXXCO

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2004241188	A1	20041202	US 2004-789400	20040227
AU 2004262624	A1	20050217	AU 2004-262624	20040227
CA 2517394	A1	20050217	CA 2004-2517394	20040227
WO 2005014626	A2	20050217	WO 2004-US5881	20040227
WO 2005014626	A3	20050428		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

EP 1603939 A2 20051214 EP 2004-775808 20040227
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK

AB The present invention relates to an isolated recombinant human metapneumovirus (rHMPV), comprising a partial or complete, recombinant HMPV genome or antigenome comprising one or more attenuating nucleotide modifications, and a major nucleocapsid protein, a nucleocapsid phosphoprotein (P), and a large polymerase protein (L). The rHMPVs, including chimeric and chimeric HMPV vectors viruses, provided according to the current disclosure are infectious and attenuated in permissive mammalian subjects, including humans. The rHMPVs are useful in immunogenic compns. for eliciting an immune response against HPIV, against one or more non-HMPV pathogens, or against a HMPV and a non-HMPV pathogen. Also provided are isolated polynucleotide mols. and vectors incorporating a recombinant HMPV genome of antigenome.

L4 ANSWER 6 OF 10 MEDLINE on STN DUPLICATE 3

AU Ishiguro Nobuhisa; Ebihara Takashi; Endo Rika; Ma Xiaoming; Kikuta Hideaki; Ishiko Hiroaki; Kobayashi Kunihiko

TI High genetic diversity of the attachment (G) protein of human metapneumovirus.

SO Journal of clinical microbiology, (2004 Aug) Vol. 42, No. 8, pp. 3406-14. Journal code: 7505564. ISSN: 0095-1137.

AB Complete genes encoding the predicted nucleoprotein (N), phosphoprotein (P), matrix protein (M), fusion protein (F), M2-1protein, M2-2protein, small hydrophobic protein (SH), and attachmentprotein (G) of seven newly isolated human metapneumoviruses (hMPVs) were analyzed and compared with previously published data for hMPV genes. Phylogenetic analysis of the nucleotide sequences indicated that there were two genetic groups, tentatively named groups 1 and 2, similar to the grouping of human respiratory syncytial virus. Although the predicted amino acid sequences of N, P, M, F, and M2 were highly conserved between the two groups (amino acid identities, 96% for N, 85% for P, 97% for M, 94% for F, 95% for M2-1, and 90% for M2-2), the amino acid identities of the SH and G proteins were low (SH, 58%; G, 33%). Furthermore, each group could be subdivided into two subgroups by phylogenetic analysis, tentatively named subgroups 1A and 1B and subgroups 2A and 2B. The predicted amino acid sequences of G within members of each subgroup were highly conserved (amino acid identities, 88% for group 1A, 93% for group 1B, and 96% for group 2B). The G of hMPV is thought to be the major antigenic determinant and to play an important role in the production of neutralizing antibodies. Clarification of the antigenic diversity of G is important for epidemiological analysis and for establishment of strategies to prevent hMPV infection.

L4 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN

IN Haller, Aurelia; Tang, Roderick; Fouchier, Ronaldus Adrianus Maria; Van den Hoogen, Bernadetta Gerarda; Osterhaus, Albertus Dominicus Marcellinus Erasmus

TI Recombinant or chimeric virus encoding human Metapneumovirus N, M, F, L, P, M2-1, M2-2, SH or G ORFs for use as vaccines and diagnostic agent

SO PCT Int. Appl., 568 pp.
CODEN: PIXXD2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2003072719	A2	20030904	WO 2003-US5271	20030221
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2477234	A1	20030904	CA 2003-2477234	20030221
AU 2003219837	A1	20030909	AU 2003-219837	20030221
US 2003232326	A1	20031218	US 2003-371099	20030221
US 2004005545	A1	20040108	US 2003-373567	20030221
CN 1646684	A	20050727	CN 2003-808914	20030221
EP 1576090	A2	20050921	EP 2003-716116	20030221
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
JP 2006500907	T	20060112	JP 2003-571407	20030221

AB The present invention provides an isolated mammalian neg. strand RNA virus, metapneumovirus (MPV), within the sub-family Pneumoviridae, of the family Paramyxoviridae. The invention also provides isolated mammalian

neg. strand RNA viruses identifiable as phylogenetically corresponding or relating to the genus Metapneumovirus and components thereof. In particular the invention provides a mammalian MPV, subgroups and variants thereof. The invention relates to genomic nucleotide sequences of different isolates of mammalian metapneumoviruses, in particular human metapneumoviruses. The invention relates to the use of the sequence information of different isolates of mammalian metapneumoviruses for diagnostic and therapeutic methods. The present invention relates to nucleotide sequences encoding the genome of a metapneumovirus or a portion thereof, including both mammalian and avian metapneumovirus. The invention further encompasses chimeric or recombinant viruses encoded by said nucleotide sequences. The invention also relates to chimeric and recombinant mammalian MPV that comprise one or more non-native or heterologous sequences. The invention further relates to vaccine formulations comprising mammalian or avian metapneumovirus, including recombinant and chimeric forms of said viruses. The vaccine preparation of the invention encompass multivalent vaccines, including bivalent and trivalent vaccine prepns.

L4 ANSWER 8 OF 10 MEDLINE on STN DUPLICATE 4
AU Jacobs Janet Ashley; Njenga M Kariuki; Alvarez Rene; Mawditt Karen; Britton Paul; Cavanagh Dave; Seal Bruce S
TI Subtype B avian metapneumovirus resembles subtype A more closely than subtype C or human metapneumovirus with respect to the phosphoprotein, and second matrix and small hydrophobic proteins.
SO Virus research, (2003 Apr) Vol. 92, No. 2, pp. 171-8.
Journal code: 8410979. ISSN: 0168-1702.
AB Avian metapneumovirus (aMPV) subtype B (aMPV/B) nucleotide sequences were obtained for the phosphoprotein (P), second matrix protein (M2), and small hydrophobic protein (SH) genes. By comparison with sequences from other metapneumoviruses, aMPV/B was most similar to subtype A aMPV (aMPV/A) relative to the US subtype C isolates (aMPV/C) and human metapneumovirus (hMPV). Strictly conserved residues common to all members of the Pneumovirinae were identified in the predicted amino acid sequences of the P and M2 protein-predicted amino acid sequences. The Cys(3)-His(1) motif, thought to be important for binding zinc, was also present in the aMPV M2 predicted protein sequences. For both the P and M2-1 protein-predicted amino acid sequences, aMPV/B was most similar to aMPV/A (72 and 89% identity, respectively), having only approximately 52 and 70% identity, respectively, relative to aMPV/C and hMPV. Differences were more marked in the M2-2 proteins, subtype B having 64% identity with subtype A but < or = 25% identity with subtype C and hMPV. The A and B subtypes of aMPV had predicted amino acid sequence identities for the SH protein of 47%, and less than 20% with that of hMPV. An SH gene was not detected in the aMPV/C. Phylogenetically, aMPV/B clustered with aMPV/A, while aMPV/C grouped with hMPV.

L4 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AU Biacchesi, Stephane; Skiadopoulos, Mario H.; Boivin, Guy; Hanson, Christopher T.; Murphy, Brian R.; Collins, Peter L.; Buchholz, Ursula J.
TI Genetic diversity between human metapneumovirus subgroups
SO Virology (2003), 315(1), 1-9
CODEN: VIRLAX; ISSN: 0042-6822
AB Complete consensus nucleotide sequences were determined for human metapneumovirus (HMPV) isolates CAN97-83 and CAN98-75, representing the two proposed genotypes or genetic subgroups of HMPV. The overall level of genome nucleotide sequence identity and aggregate proteome amino acid sequence identity between the two HMPV subgroups were 80 and 90%, resp., similar to the resp. values of 81 and 88% between the two antigenic subgroups of human respiratory syncytial virus (HRSV). The diversity between HMPV subgroups was greatest for the SH and G proteins (59 and 37% identity, resp.), which were even more divergent than their HRSV counterparts (72 and 55% cross-subgroup identity, resp.). It is reasonable to anticipate that the two genetic subgroups of HMPV represent

antigenic subgroups approx. comparable to those of HRSV.

L4 ANSWER 10 OF 10 MEDLINE on STN DUPLICATE 5
AU van den Hoogen Bernadette G; Bestebroer Theo M; Osterhaus Albert D M E; Fouchier Ron A M
TI Analysis of the genomic sequence of a human metapneumovirus.
SO Virology, (2002 Mar 30) Vol. 295, No. 1, pp. 119-32.
Journal code: 0110674. ISSN: 0042-6822.
AB We recently described the isolation of a novel paramyxovirus from children with respiratory tract disease in The Netherlands. Based on biological properties and limited sequence information the virus was provisionally classified as the first nonavian member of the Metapneumovirus genus and named human metapneumovirus (hMPV). This report describes the analysis of the sequences of all hMPV open reading frames (ORFs) and intergenic sequences as well as partial sequences of the genomic termini. The overall percentage of amino acid sequence identity between APV and hMPV N, P, M, F, M2-1, M2-2, and L ORFs was 56 to 88%. Some nucleotide sequence identity was also found between the noncoding regions of the APV and hMPV genomes. Although no discernible amino acid sequence identity was found between two of the ORFs of hMPV and ORFs of other paramyxoviruses, the amino acid content, hydrophilicity profiles, and location of these ORFs in the viral genome suggest that they represent SH and G proteins. The high percentage of sequence identity between APV and hMPV, their similar genomic organization (3'-N-P-M-F-M2-SH-G-L-5'), and phylogenetic analyses provide evidence for the proposed classification of hMPV as the first mammalian metapneumovirus.

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